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NOVEL HUMAN TRYPSIN FAMILY MEMBER AND THEREOF
Rachel Meyers et al.
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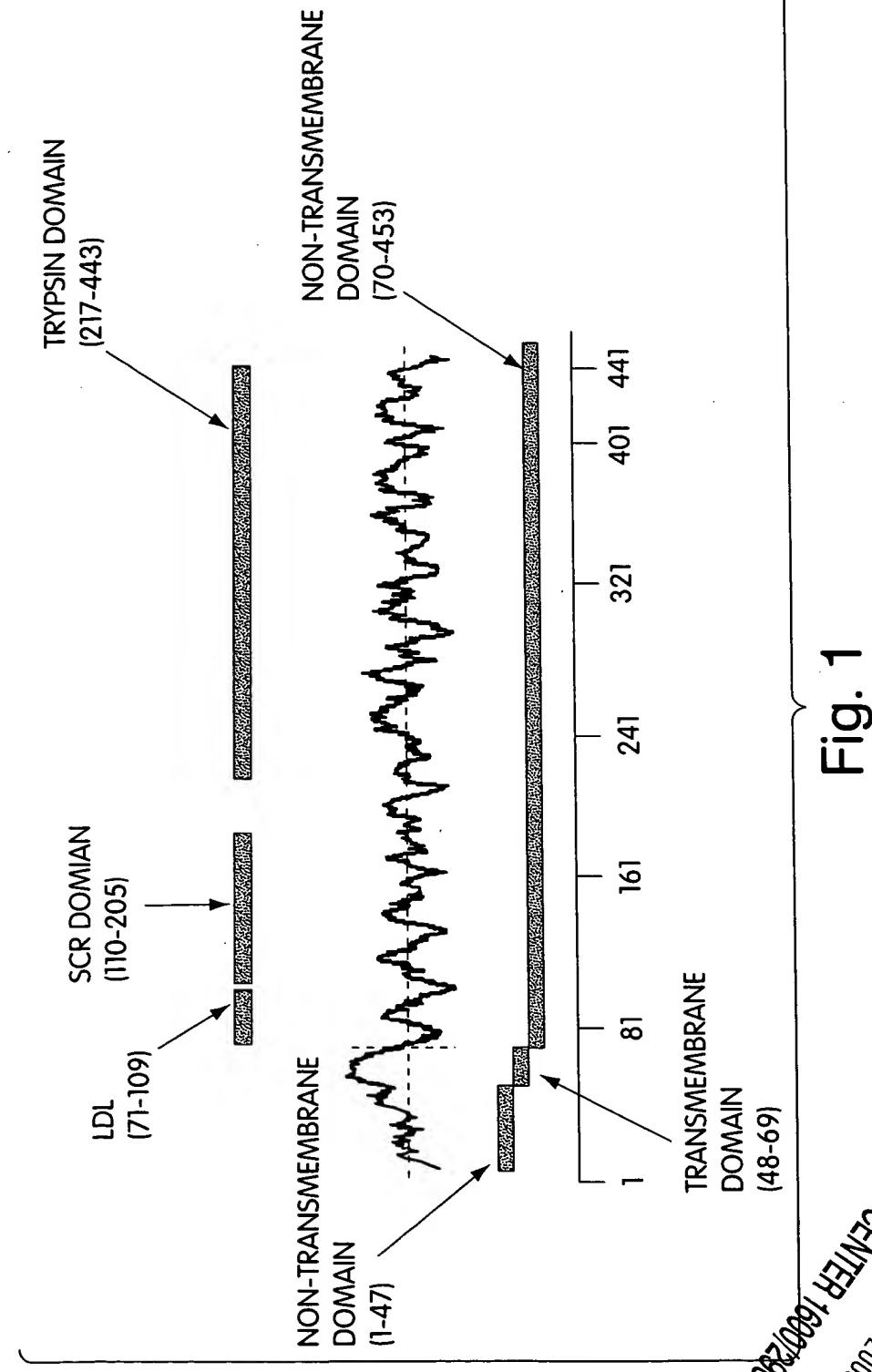


Fig. 1

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trypsin: domain 1 of 1, from 217 to 443: score 293.0, E = 3.2e-92
 *->IvGGreapqgsfPwqvs1qvrsgggsrkhfCGGsLisenwVLTAA
 IvGG + ++ Pwq+slq+ + +h+CGGs+i + w++TAA
 14094 217 IVGGNMSLLSQW--PWQASLQFQG----YHLCGGSVITPLWIITAA 256

HCvsgaasapassvrVSlsvrlGehnlslteqkfdvkktiivHpnyn
 HCv++ + + + S++ + G + sl + v+k i+ H++y
 14094 257 HCVYD--LYLPKSWTI---QVGL--VSLLDNPAPSHLVEK-IVYHSKYK 297

pdtldnngaYdnDiALLkLkspgvtlgdtvrpicLpsassdlpvGttctvs
 p+ l+ nDiAL+kL++p +t++ + +p+cLp + + +p+G c+ s
 14094 298 PKRLG----NDIALMKGAP-LTFNEMIQPVCLPNSEENFPDGKVCWTS 341

GwGrrptknlg.lsdtLqevvvvvvretCrsayeyggdDkvefvtdnm
 GwG t+++g+ s +L ++ vp++s++ C+++ ygg + + + m
 14094 342 GWGA--TEDGGdASPVLNHAAPVLISNKICNHRDVYGGI----ISPSM 383

iCagal.ggkdaCqGDSGGPLvcsgndgrwelvGivSwGsygCargnk
 +Cag+l+gg+d+CqGDSGGPLvc w+lvG +S+G gCa+ nk
 14094 384 LCAGYLtGGVDSCQGDSGGPLVCQER--RLWKLVGATSFG-IGCAEVNK 429

PGvytrVssyldWI--*
 PGvytrV+s+ldWI
 14094 430 PGVYTRVTSFLDWI 443

Fig. 2A

trypsin_2: domain 1 of 1, from 216 to 443: score 328.2, E = 9.2e-95
 *->RIVGGseakigsfPWqvsLq.....CGGSLIsprwVLTAHC....
 RIVGG+ + ++PWq+slq ++ + CGGS+I+p w++TAHC +
 14094 216 RIVGGNMSLLSQWPWQASLQfqqyh1CGGSVITPLWIITAAHCvydl 262

.....rVrlGshdlssgeeteggprldspggqvikVskiieVHpnYn..
 + + + +G +l + + + + V+ki+ H +Y ++
 14094 263 ylpkswTIQVGLVSLLDNP-----APSHLVEKIV-YHSKYKpk 299

...NDIALLkLkeptvlsdsntvrPicLPssneiktsegntvpaGttctV
 + +NDIAL+kL+ p+t++ + +P+cLp+s + + +p+G c+
 14094 300 rlgNDIALMKGAPLTFNE--MIQPVCLPNS-----EENFPDGKVCWT 340

sGWGrtsegpeesgggslpdvLqevnvpiwsnetCr.....Ml
 sGWG t++ gg + vL ++ vp++sn+ C++++ + + + + + +Ml
 14094 341 SGWGATED-----GGDASPVLNHAAPVLISNKICNhrdvyyggiispsML 384

CAGyleggntpgGkDaCqGDSGGPLvc.....vLvGiVSWGssslygCa
 CAGyl+ gG+D+CqGDSGGPLvc++++ + +LvG +S+G +gCa
 14094 385 CAGYLT----GGVDSCQGDSGGPLVCqerrlwKLVGATSFG---IGCA 425

rpnkPGVYTrVssyldWI--*
 + nkPGVYTrV+s+ldWI
 14094 426 EVNKGPGVYTRVTSFLDWI 443

Fig. 2B

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BEGIN SEQ ID NO: 6 → END SEQ ID NO: 6 ↓
->stCggpdeFqCgsgrCIprswvCDGdpDCeDGSDEslenCaa<-
+C+ +++C+s+ CI +CDG DC+DG+DE +C++
14094 71 FDGS--GKYRCRSSFKCIELIARCDGVSDCKDGEDE--YRCVR 109

Fig. 3A

↓ BEGIN SEQ ID NO: 7
*->vgGssrCeGrVEVrhgskWgtVCdssWslrdanvdpQaskvCrqLG
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14094 110 VGG--QNA-VLQVF-TAASWKTMCSDDWKGHYANV-----ACAQLG 146

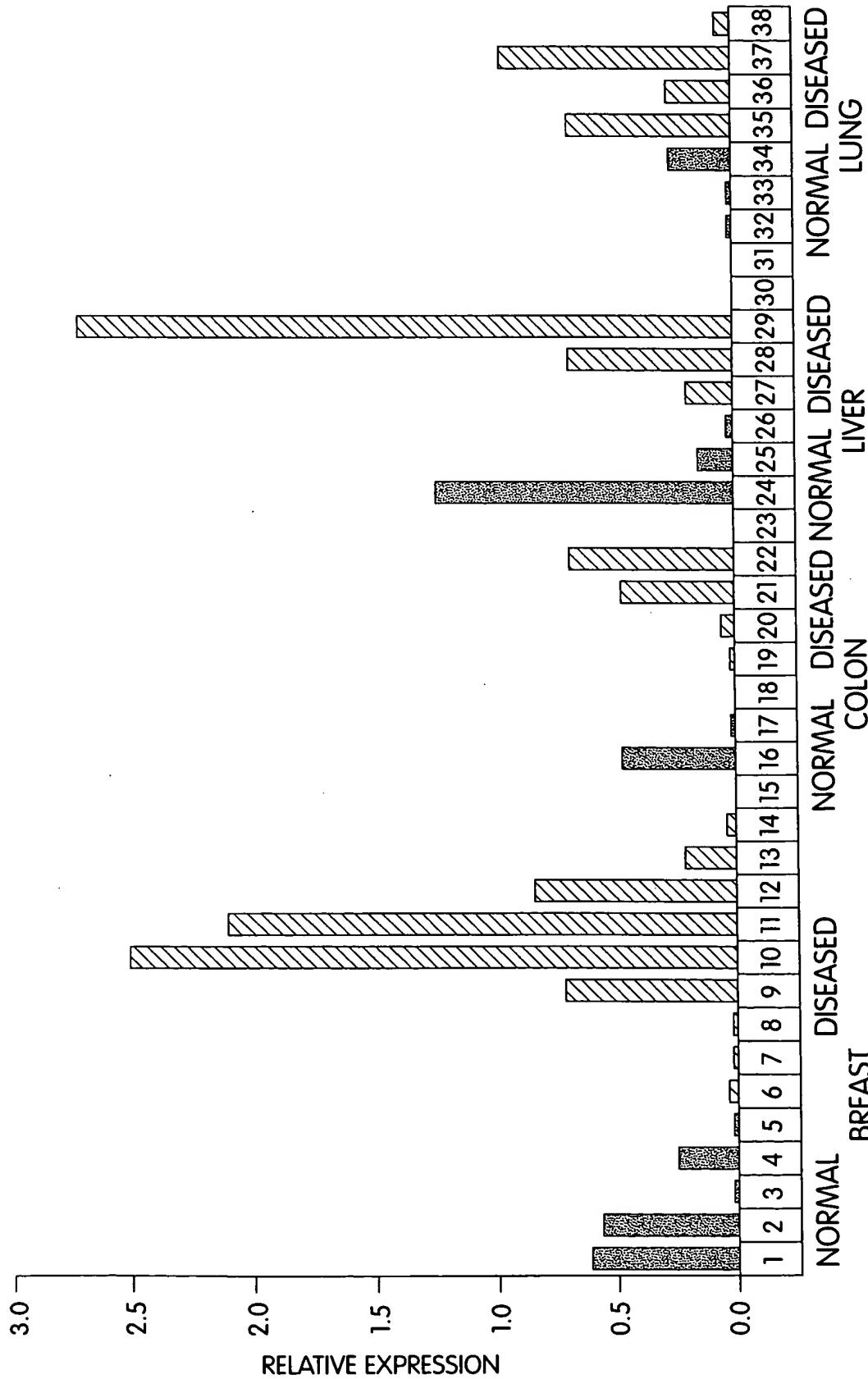
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+ vs+ + s+ g ++++++ + +++++ +++
14094 147 FPSYVSSDnLRVSSLEG-----QFREEFVSIDHllpdDKVTALHHS-- 187

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Fig. 3B



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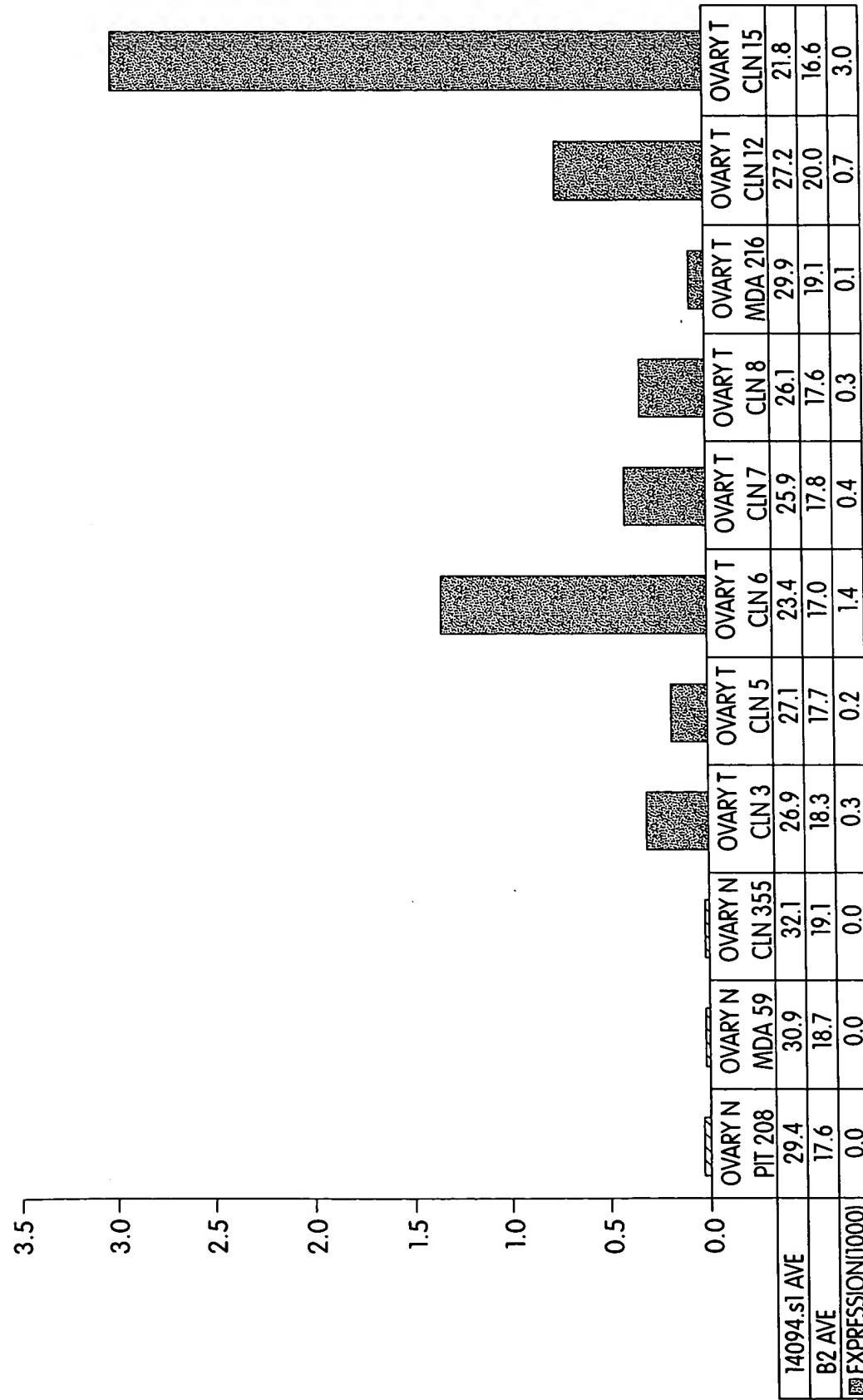


Fig. 5



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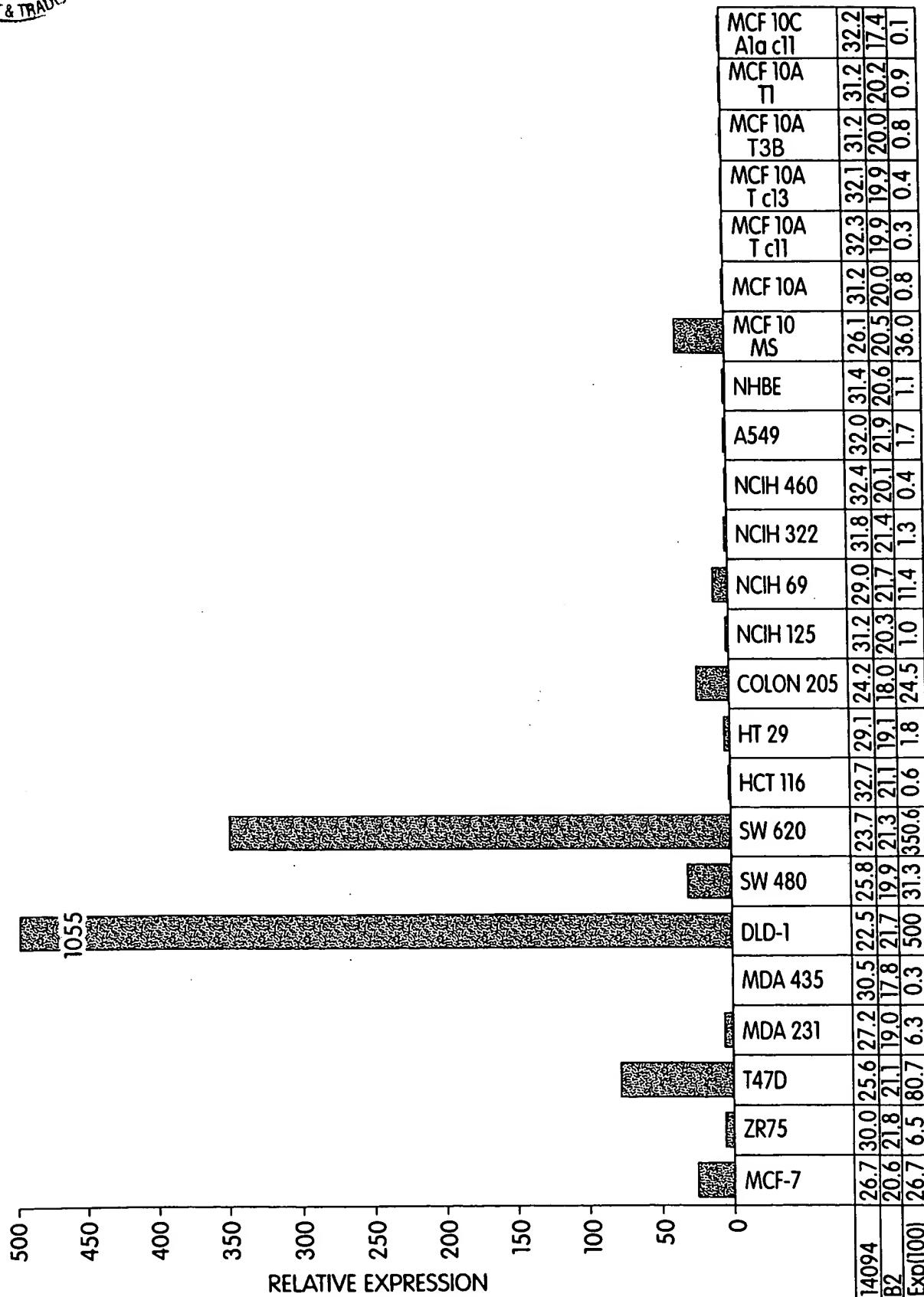


Fig. 6